

FIG. 1B

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_	GTTTTCAAAA	DUADULDUJI	AAAATITAAAA	A(+ A (-(-(-(-(-(-(-(-(-(-(-(-(-(-(-(-(-(

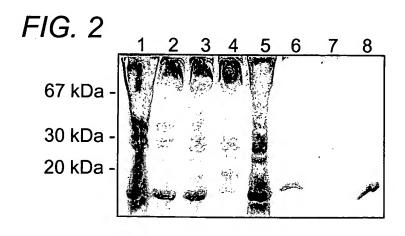
- 41 CATTTTTGA AAATAAAAA ATATCAATAA GTTGGAGTCA ↓START
- 81 <u>TTACCG</u>AATT TTTATACTTA TTTGTT<u>TAGA ATGAACTTTA</u>
 -35
- 121 TAACATAGTT GGATAGAGTT TTCGATTTAA TACATTAAAT
- 161 GTGAACCTTG CTACAACAAG ATGTGCATCA GA<u>AGGAGTGG</u>
 RIBOSOME BINDING SITE
- 201 TTTAATAATG --sarR--TAA (SEQ ID NO:19)

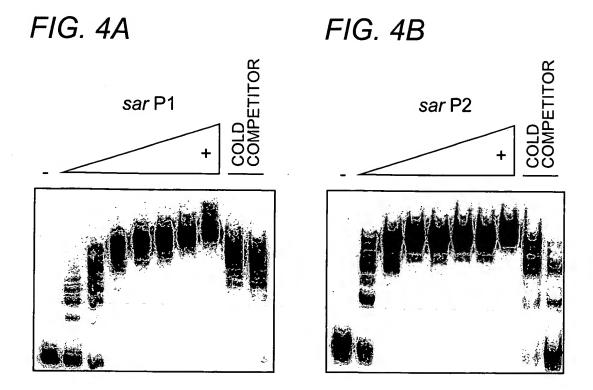
FIG. 1C

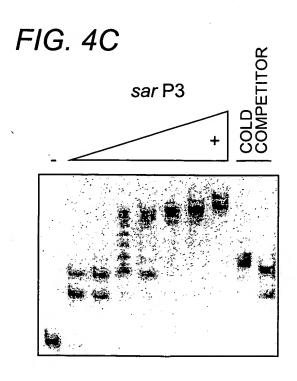
50 60 70 80
SarR HILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLS
.:..: .:. .:. .:.
SarA YISENKEKEYYLKDIINHLNYKQPQVVKAVKILSQEDYFD

SarR IKN (SEQ ID NO:2)

SarA IEL (SEQ ID NO:3)







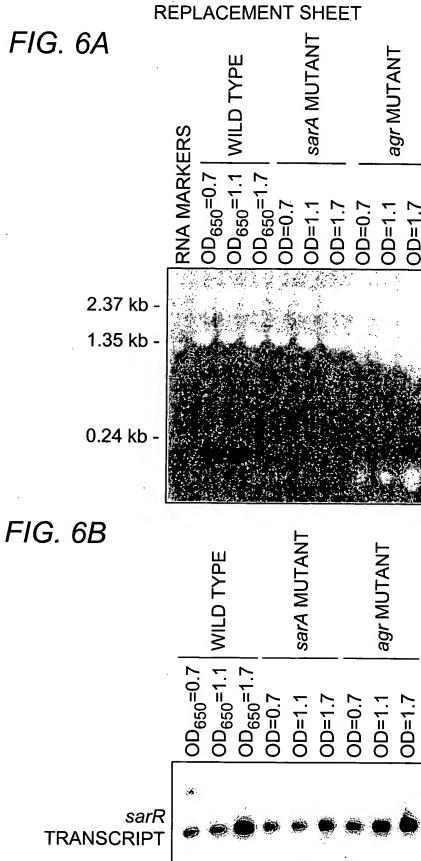


FIG. 9A

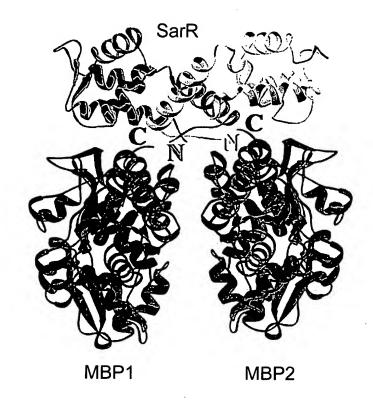
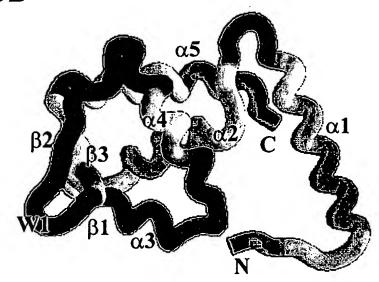
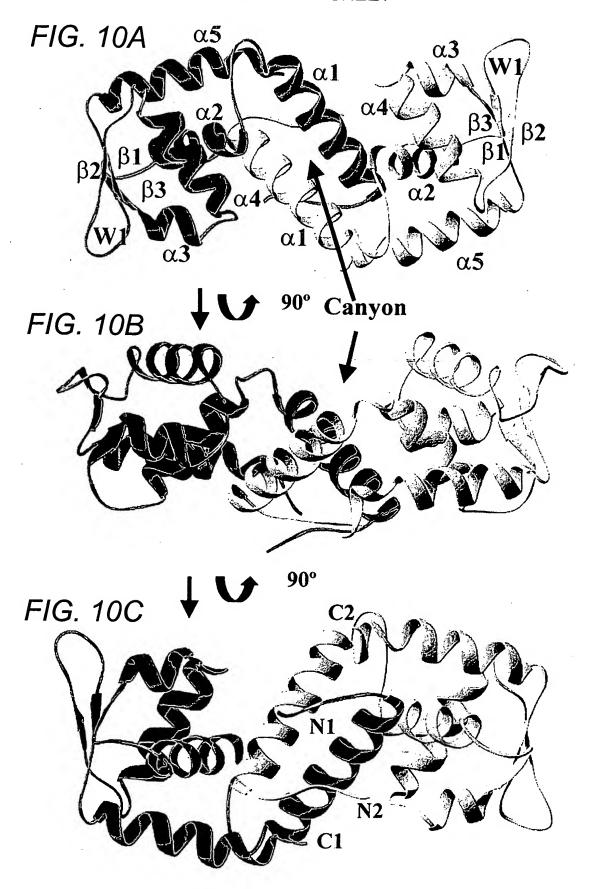


FIG. 9B





X N X (SEQ ID NO:26) MAJORITY 119 F N - (SEQ ID NO:27) SarS1 118 - K D (SEQ ID NO:28) SarS2 119 A N (SEQ ID NO:35) SarA 117 - - - (SEQ ID NO:2) SarR

FIG. 12A

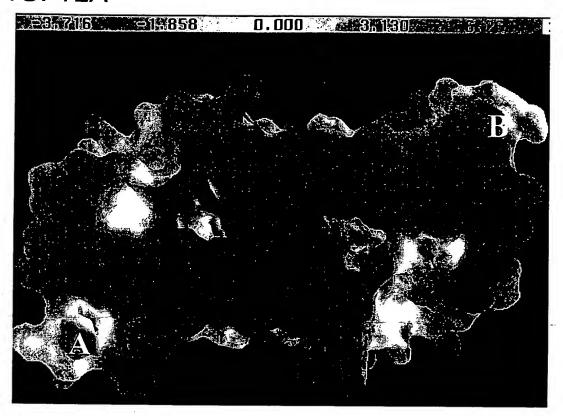


FIG. 12B



